

10/581570

SEQUENCE LISTING

AP20 Rec'd PCT/PTO 02 JUN 2006

<110> Liao et al.

<120> PRODUCTION OF 3-HYDROXYPROPIONIC ACID USING BETA
-ALANINE/PYRUVATE AMINOTRANSFERASE

<130> 66576-05

<150> PCT/US2004/040827

<151> 2004-12-06

<150> US 60/527,357

<151> 2003-12-04

<160> 28

<170> PatentIn version 3.2

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ctg gac gcc cac tgg atg ccc tac acc gcc aac cgc aac ttc cag cgc      96
Leu Asp Ala His Trp Met Pro Tyr Thr Ala Asn Arg Asn Phe Gln Arg
          20          25          30

gac cca cgc ctg atc gtg gcg gcc gaa ggc aac tac ctg gtc gat gac      144
Asp Pro Arg Leu Ile Val Ala Ala Glu Gly Asn Tyr Leu Val Asp Asp
          35          40          45

cac ggg cgc aag atc ttc gac gcc ctg tcc ggc ctg tgg acc tgc ggc      192
His Gly Arg Lys Ile Phe Asp Ala Leu Ser Gly Leu Trp Thr Cys Gly
          50          55          60

gca ggg cac act cgc aag gaa atc gct gac gcg gtg acc cgt caa ctg      240
Ala Gly His Thr Arg Lys Glu Ile Ala Asp Ala Val Thr Arg Gln Leu
65          70          75          80

agt acg ctg gac tac tcc cca gcg ttc cag ttc ggc cac ccg ctg tcg      288
Ser Thr Leu Asp Tyr Ser Pro Ala Phe Gln Phe Gly His Pro Leu Ser
          85          90          95

ttc cag ctg gcg gaa aag atc gcc gag ctg gtt ccg ggc aat ctg aat      336
Phe Gln Leu Ala Glu Lys Ile Ala Glu Leu Val Pro Gly Asn Leu Asn
          100          105          110

cac gtc ttc tat acc aac tcc ggt tcc gag tgc gcc gat acc gca ctg      384
His Val Phe Tyr Thr Asn Ser Gly Ser Glu Cys Ala Asp Thr Ala Leu
          115          120          125

aag atg gtg cgt gcc tac tgg cgc ctg aaa ggc cag gca acc aag acc      432
Lys Met Val Arg Ala Tyr Trp Arg Leu Lys Gly Gln Ala Thr Lys Thr
          130          135          140

aag atc atc ggc cgt gcc cgt ggt tac cat ggc gtg aac atc gcc ggt      480
Lys Ile Ile Gly Arg Ala Arg Gly Tyr His Gly Val Asn Ile Ala Gly
145          150          155          160

acc agc ctg ggt ggc gtc aac ggt aac cgc aag atg ttt ggc cag ctg      528
Thr Ser Leu Gly Gly Val Asn Gly Asn Arg Lys Met Phe Gly Gln Leu
          165          170          175

ctg gac gtc gac cac ctg cct cac act gta ttg ccg gtg aac gcc ttc      576
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          180          185          190

tcg aaa ggc ttg ccg gaa gag ggc ggt atc gcg ctg gct gac gaa atg      624
Ser Lys Gly Leu Pro Glu Glu Gly Gly Ile Ala Leu Ala Asp Glu Met
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Tyr	Leu	Lys	Arg	Leu	Arg	Glu	Ile	Cys	Thr	Gln	His	Asn	Ile	Leu	Leu	
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Gly	Ser	Glu	Ala	Phe	Gly	Val	Thr	Pro	Asp	Leu	Met	Cys	Ile	Ala	Lys	
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Gln	Val	Thr	Asn	Gly	Ala	Ile	Pro	Met	Gly	Ala	Val	Ile	Ala	Ser	Ser	
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gag	atc	tac	cag	acc	ttc	atg	aac	cag	ccg	acc	ccg	gaa	tac	gcc	gtg	960
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Glu	Phe	Pro	His	Gly	Tyr	Thr	Tyr	Ser	Ala	His	Pro	Val	Ala	Cys	Ala	
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Lys	Gly	Thr	Lys	Asn	Ile	Val	Asp	Ile	Arg	Asn	Tyr	Gly	Leu	Ala	Gly	
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Gly	Asp	Thr	Leu	Gln	Phe	Gly	Pro	Thr	Phe	Asn	Thr	Lys	Pro	Gln	Glu	
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tga 1347

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 <212> PRT
 <213> Pseudomonas putida

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 35 40 45

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 50 55 60

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 65 70 75 80

Ser Thr Leu Asp Tyr Ser Pro Ala Phe Gln Phe Gly His Pro Leu Ser
 85 90 95

Phe Gln Leu Ala Glu Lys Ile Ala Glu Leu Val Pro Gly Asn Leu Asn
 100 105 110

His Val Phe Tyr Thr Asn Ser Gly Ser Glu Cys Ala Asp Thr Ala Leu
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Lys Met Val Arg Ala Tyr Trp Arg Leu Lys Gly Gln Ala Thr Lys Thr
 130 135 140

Lys Ile Ile Gly Arg Ala Arg Gly Tyr His Gly Val Asn Ile Ala Gly
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Glu	Ala	Ala	Met	Lys	Leu	Trp	Lys	Ala	Gly	Phe	Tyr	Val	Arg	Phe	Gly
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Leu Arg Ala His Trp Met Pro Phe Ser Ala Asn Arg Asn Phe Gln Lys
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Asp Pro Arg Ile Ile Val Ala Ala Glu Gly Ser Trp Leu Thr Asp Asp
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ggc acc ctc gac tac tcg ccg ggc ttc cag tac ggc cat ccg ctg tcc 288
Gly Thr Leu Asp Tyr Ser Pro Gly Phe Gln Tyr Gly His Pro Leu Ser
85 90 95
ttc cag ttg gcc gag aag atc gcc ggg ttg ctg cca ggc gaa ctg aac 336
Phe Gln Leu Ala Glu Lys Ile Ala Gly Leu Leu Pro Gly Glu Leu Asn
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cac gtg ttc ttc acc ggt tcc ggc tcc gag tgc gcc gac acc tcg atc 384
His Val Phe Phe Thr Gly Ser Gly Ser Glu Cys Ala Asp Thr Ser Ile
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Thr Ser Leu Gly Gly Ile Gly Gly Asn Arg Lys Met Phe Gly Gln Leu	
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Thr Arg Gly Met Ala Gln Thr Gly Gly Val Glu Leu Ala Asn Glu Leu	
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 Gly Asp Thr Leu Gln Phe Gly Pro Thr Phe Asn Ala Arg Pro Glu Glu
 420 425 430

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tga 1347

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Lys Gly Arg Lys Val Tyr Asp Ser Leu Ser Gly Leu Trp Thr Cys Gly
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Ala Gly His Ser Arg Lys Glu Ile Gln Glu Ala Val Ala Arg Gln Leu
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Gly Thr Leu Asp Tyr Ser Pro Gly Phe Gln Tyr Gly His Pro Leu Ser
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Phe Gln Leu Ala Glu Lys Ile Ala Gly Leu Leu Pro Gly Glu Leu Asn
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His Val Phe Phe Thr Gly Ser Gly Ser Glu Cys Ala Asp Thr Ser Ile
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Lys Met Ala Arg Ala Tyr Trp Arg Leu Lys Gly Gln Pro Gln Lys Thr
130 135 140

Lys Leu Ile Gly Arg Ala Arg Gly Tyr His Gly Val Asn Val Ala Gly
145 150 155 160

Thr Ser Leu Gly Gly Ile Gly Gly Asn Arg Lys Met Phe Gly Gln Leu
165 170 175

Met Asp Val Asp His Leu Pro His Thr Leu Gln Pro Gly Met Ala Phe
180 185 190

Thr Arg Gly Met Ala Gln Thr Gly Gly Val Glu Leu Ala Asn Glu Leu
195 200 205

Leu Lys Leu Ile Glu Leu His Asp Ala Ser Asn Ile Ala Ala Val Ile
210 215 220

Val Glu Pro Met Ser Gly Ser Ala Gly Val Leu Val Pro Pro Val Gly
225 230 235 240

Tyr Leu Gln Arg Leu Arg Glu Ile Cys Asp Gln His Asn Ile Leu Leu
245 250 255

Ile Phe Asp Glu Val Ile Thr Ala Phe Gly Arg Leu Gly Thr Tyr Ser
260 265 270

Gly Ala Glu Tyr Phe Gly Val Thr Pro Asp Leu Met Asn Val Ala Lys
275 280 285

Gln Val Thr Asn Gly Ala Val Pro Met Gly Ala Val Ile Ala Ser Ser
290 295 300

Glu Ile Tyr Asp Thr Phe Met Asn Gln Ala Leu Pro Glu His Ala Val
305 310 315 320

Glu Phe Ser His Gly Tyr Thr Tyr Ser Ala His Pro Val Ala Cys Ala
325 330 335

Ala Gly Leu Ala Ala Leu Asp Ile Leu Ala Arg Asp Asn Leu Val Gln

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Gln Gly Ala Lys Asn Val Ile Asp Ile Arg Asn Cys Gly Leu Ala Gly		
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Ala Ile Gln Ile Ala Pro Arg Asp Gly Asp Pro Thr Val Arg Pro Phe		
385	390	395
Glu Ala Gly Met Lys Leu Trp Gln Gln Gly Phe Tyr Val Arg Phe Gly		
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Gly Asp Thr Leu Gln Phe Gly Pro Thr Phe Asn Ala Arg Pro Glu Glu		
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Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln	
20 25 30	
ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat	144
Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn	
35 40 45	
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Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn	
65 70 75 80	

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Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met	
85 90 95	
cac aaa aca aaa tac gat atg gaa gac ccg ctt cat gag gat gaa gat	336
His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp	
100 105 110	
tca ccg gta ccc ggt ctg aca cac cgc tat ccc gac cgt gtg ctg ttt	384
Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe	
115 120 125	
ctt gtc acg aat caa tgt tcc gtg tac tgc cgc cac tgc aca cgc cgg	432
Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg His Cys Thr Arg Arg	
130 135 140	
cgc ttt tcc gga caa atc gga atg ggc gtc ccc aaa aaa cag ctt gat	480
Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp	
145 150 155 160	
gct gca att gct tat atc cgg gaa aca ccc gaa atc cgc gat tgt tta	528
Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu	
165 170 175	
att tca ggc ggt gat ggg ctg ctc atc aac gac caa att tta gaa tat	576
Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr	
180 185 190	
att tta aaa gag ctg cgc agc att ccg cat ctg gaa gtc atc cgc atc	624
Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile	
195 200 205	
gga aca cgt gct ccc gtc gtc ttt ccg cag cgc att acc gat cat ctg	672
Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu	
210 215 220	
tgc gag ata ttg aaa aaa tat cat ccg gtc tgg ctg aac acc cat ttt	720
Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe	
225 230 235 240	
aac aca agc atc gaa atg aca gaa gaa tcc gtt gag gca tgt gaa aag	768
Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys	
245 250 255	
ctg gtg aac gcg gga gtg ccg gtc gga aat cag gct gtc gta tta gca	816
Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala	
260 265 270	
ggt att aat gat tcg gtt cca att atg aaa aag ctc atg cat gac ttg	864
Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu	
275 280 285	
gta aaa atc aga gtc cgt cct tat tat att tac caa tgt gat ctg tca	912
Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser	
290 295 300	

gaa gga ata ggg cat ttc cgt gct cct gtt tcc aaa ggt ttg gag atc	960
Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile	
305 310 315 320	
att gaa ggg ctg aga ggt cat acc tca ggc tat gcg gtt cct acc ttt	1008
Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe	
325 330 335	
gtc gtt cac gca cca ggc gga gga ggt aaa atc gcc ctg cag ccg aac	1056
Val Val His Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn	
340 345 350	
tat gtc ctg tca caa agt cct gac aaa gtg atc tta aga aat ttt gaa	1104
Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu	
355 360 365	
ggg gtg att acg tca tat ccg gaa cca gag aat tat atc ccc aat cag	1152
Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln	
370 375 380	
gca gac gcc tat ttt gag tcc gtt ttc cct gaa acc gct gac aaa aag	1200
Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys	
385 390 395 400	
gag ccg atc ggg ctg agt gcc att ttt gct gac aaa gaa gtt tcg ttt	1248
Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe	
405 410 415	
aca cct gaa aat gta gac aga atc aaa cgg cgt gag gca tac atc gca	1296
Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala	
420 425 430	
aat ccg gag cat gaa aca tta aaa gat cgg cgt gag aaa aga gat cag	1344
Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln	
435 440 445	
ctc aaa gaa aag aaa ttt ttg gcg cag cag aaa aaa cag aaa gag act	1392
Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr	
450 455 460	
gaa tgc gga ggg gat tct tca tga	1416
Glu Cys Gly Gly Asp Ser Ser	
465 470	

<210> 22

<211> 471

<212> PRT

<213> Bacillus subtilis

<400> 22

Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu
1 5 10 15

Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln

	20		25		30	
Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn	35		40		45	
Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile	50		55		60	
Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn	65		70		75	80
Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met		85		90		95
His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp		100		105		110
Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe		115		120		125
Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg His Cys Thr Arg Arg		130		135		140
Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp		145		150		155
						160
Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu		165		170		175
Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr		180		185		190
Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile		195		200		205
Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu		210		215		220
Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe		225		230		235
						240
Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys		245		250		255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala
260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu
275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser
290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile
305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe
325 330 335

Val Val His Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn
340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu
355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln
370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys
385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe
405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala
420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln
435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr
450 455 460

Glu Cys Gly Gly Asp Ser Ser
465 470

<210> 23
 <211> 1416
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(1413)

<400> 23
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 Met Lys Asn Lys Trp Tyr Lys Pro Lys Arg His Trp Lys Glu Ile Glu
 1 5 10 15
 tta tgg aag gac gtt ccg gaa gag aaa tgg aac gat tgg ctt tgg cag 96
 Leu Trp Lys Asp Val Pro Glu Glu Lys Trp Asn Asp Trp Leu Trp Gln
 20 25 30
 ctg aca cac act gta aga acg tta gat gat tta aag aaa gtc att aat 144
 Leu Thr His Thr Val Arg Thr Leu Asp Asp Leu Lys Lys Val Ile Asn
 35 40 45
 ctg acc gag gat gaa gag gaa ggc gtc aga att tct acc aaa acg atc 192
 Leu Thr Glu Asp Glu Glu Glu Gly Val Arg Ile Ser Thr Lys Thr Ile
 50 55 60
 ccc tta aat att aca cct tac tat gct tct tta atg gac ccc gac aat 240
 Pro Leu Asn Ile Thr Pro Tyr Tyr Ala Ser Leu Met Asp Pro Asp Asn
 65 70 75 80
 ccg aga tgc ccg gta cgc atg cag tct gtg ccg ctt tct gaa gaa atg 288
 Pro Arg Cys Pro Val Arg Met Gln Ser Val Pro Leu Ser Glu Glu Met
 85 90 95
 cac aaa aca aaa tac gat atg gaa gac ccg ctt cat gag gat gaa gat 336
 His Lys Thr Lys Tyr Asp Met Glu Asp Pro Leu His Glu Asp Glu Asp
 100 105 110
 tca ccg gta ccc ggt ctg aca cac cgc tat ccc gac cgt gtg ctg ttt 384
 Ser Pro Val Pro Gly Leu Thr His Arg Tyr Pro Asp Arg Val Leu Phe
 115 120 125
 ctt gtc acg aat caa tgt tcc gtg tac tgc cgc tac tgc aca aga agg 432
 Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg Tyr Cys Thr Arg Arg
 130 135 140
 cgc ttt tcc gga caa atc gga atg ggc gtc ccc aaa aaa cag ctt gat 480
 Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
 145 150 155 160
 gct gca att gct tat atc cgg gaa aca ccc gaa atc cgc gat tgt tta 528
 Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
 165 170 175
 att tca ggc ggt gat ggg ctg ctc atc aac gac caa att tta gaa tat 576

Ile	Ser	Gly	Gly	Asp	Gly	Leu	Leu	Ile	Asn	Asp	Gln	Ile	Leu	Glu	Tyr	
			180					185					190			
att	tta	aaa	gag	ctg	cgc	agc	att	ccg	cat	ctg	gaa	gtc	atc	aga	atc	624
Ile	Leu	Lys	Glu	Leu	Arg	Ser	Ile	Pro	His	Leu	Glu	Val	Ile	Arg	Ile	
		195					200					205				
gga	aca	aga	gct	ccc	gtc	gtc	ttt	ccg	cag	cgc	att	acc	gat	cat	ctg	672
Gly	Thr	Arg	Ala	Pro	Val	Val	Phe	Pro	Gln	Arg	Ile	Thr	Asp	His	Leu	
		210				215						220				
tgc	gag	ata	ttg	aaa	aaa	tat	cat	ccg	gtc	tgg	ctg	aac	acc	cat	ttt	720
Cys	Glu	Ile	Leu	Lys	Lys	Tyr	His	Pro	Val	Trp	Leu	Asn	Thr	His	Phe	
225					230					235					240	
aac	aca	agc	atc	gaa	atg	aca	gaa	gaa	tcc	gtt	gag	gca	tgt	gaa	aag	768
Asn	Thr	Ser	Ile	Glu	Met	Thr	Glu	Glu	Ser	Val	Glu	Ala	Cys	Glu	Lys	
				245					250					255		
ctg	gtg	aac	gcg	gga	gtg	ccg	gtc	gga	aat	cag	gct	gtc	gta	tta	gca	816
Leu	Val	Asn	Ala	Gly	Val	Pro	Val	Gly	Asn	Gln	Ala	Val	Val	Leu	Ala	
			260					265					270			
ggt	att	aat	gat	tcg	gtt	cca	att	atg	aaa	aag	ctc	atg	cat	gac	ttg	864
Gly	Ile	Asn	Asp	Ser	Val	Pro	Ile	Met	Lys	Lys	Leu	Met	His	Asp	Leu	
		275				280						285				
gta	aaa	atc	aga	gtc	cgt	cct	tat	tat	att	tac	caa	tgt	gat	ctg	tca	912
Val	Lys	Ile	Arg	Val	Arg	Pro	Tyr	Tyr	Ile	Tyr	Gln	Cys	Asp	Leu	Ser	
	290					295					300					
gaa	gga	ata	ggg	cat	ttc	aga	gct	cct	gtt	tcc	aaa	ggt	ttg	gag	atc	960
Glu	Gly	Ile	Gly	His	Phe	Arg	Ala	Pro	Val	Ser	Lys	Gly	Leu	Glu	Ile	
305					310					315					320	
att	gaa	ggg	ctg	aga	ggt	cat	acc	tca	ggc	tat	gcg	gtt	cct	acc	ttt	1008
Ile	Glu	Gly	Leu	Arg	Gly	His	Thr	Ser	Gly	Tyr	Ala	Val	Pro	Thr	Phe	
			325						330				335			
gtc	gtt	cac	gca	cca	ggc	gga	gga	ggt	aaa	atc	gcc	ctg	cag	ccg	aac	1056
Val	Val	His	Ala	Pro	Gly	Gly	Gly	Gly	Lys	Ile	Ala	Leu	Gln	Pro	Asn	
			340					345					350			
tat	gtc	ctg	tca	caa	agt	cct	gac	aaa	gtg	atc	tta	aga	aat	ttt	gaa	1104
Tyr	Val	Leu	Ser	Gln	Ser	Pro	Asp	Lys	Val	Ile	Leu	Arg	Asn	Phe	Glu	
		355				360						365				
ggt	gtg	att	acg	tca	tat	ccg	gaa	cca	gag	aat	tat	atc	ccc	aat	cag	1152
Gly	Val	Ile	Thr	Ser	Tyr	Pro	Glu	Pro	Glu	Asn	Tyr	Ile	Pro	Asn	Gln	
		370				375					380					
gca	gac	gcc	tat	ttt	gag	tcc	gtt	ttc	cct	gaa	acc	gct	gac	aaa	aag	1200
Ala	Asp	Ala	Tyr	Phe	Glu	Ser	Val	Phe	Pro	Glu	Thr	Ala	Asp	Lys	Lys	
385					390					395					400	
gag	ccg	atc	ggg	ctg	agt	gcc	att	ttt	gct	gac	aaa	gaa	gtt	tcg	ttt	1248
Glu	Pro	Ile	Gly	Leu	Ser	Ala	Ile	Phe	Ala	Asp	Lys	Glu	Val	Ser	Phe	

405										410					415					
aca	cct	gaa	aat	gta	gac	aga	atc	aaa	agg	aga	gag	gca	tac	atc	gca	1296				
Thr	Pro	Glu	Asn	Val	Asp	Arg	Ile	Lys	Arg	Arg	Glu	Ala	Tyr	Ile	Ala					
			420					425				430								
aat	ccg	gag	cat	gaa	aca	tta	aaa	gat	cgg	cgt	gag	aaa	aga	gat	cag	1344				
Asn	Pro	Glu	His	Glu	Thr	Leu	Lys	Asp	Arg	Arg	Glu	Lys	Arg	Asp	Gln					
			435				440					445								
ctc	aaa	gaa	aag	aaa	ttt	ttg	gcg	cag	cag	aaa	aaa	cag	aaa	gag	act	1392				
Leu	Lys	Glu	Lys	Lys	Phe	Leu	Ala	Gln	Gln	Lys	Lys	Gln	Lys	Glu	Thr					
			450			455						460								
gaa	tgc	gga	ggg	gat	tct	tca	tga									1416				
Glu	Cys	Gly	Gly	Asp	Ser	Ser														
465					470															

<210> 24
 <211> 471
 <212> PRT
 <213> Bacillus subtilis

<400> 24

Met	Lys	Asn	Lys	Trp	Tyr	Lys	Pro	Lys	Arg	His	Trp	Lys	Glu	Ile	Glu
1				5					10					15	
Leu	Trp	Lys	Asp	Val	Pro	Glu	Glu	Lys	Trp	Asn	Asp	Trp	Leu	Trp	Gln
			20					25					30		
Leu	Thr	His	Thr	Val	Arg	Thr	Leu	Asp	Asp	Leu	Lys	Lys	Val	Ile	Asn
			35				40					45			
Leu	Thr	Glu	Asp	Glu	Glu	Glu	Gly	Val	Arg	Ile	Ser	Thr	Lys	Thr	Ile
			50			55					60				
Pro	Leu	Asn	Ile	Thr	Pro	Tyr	Tyr	Ala	Ser	Leu	Met	Asp	Pro	Asp	Asn
65					70					75					80
Pro	Arg	Cys	Pro	Val	Arg	Met	Gln	Ser	Val	Pro	Leu	Ser	Glu	Glu	Met
				85					90					95	
His	Lys	Thr	Lys	Tyr	Asp	Met	Glu	Asp	Pro	Leu	His	Glu	Asp	Glu	Asp
			100					105					110		
Ser	Pro	Val	Pro	Gly	Leu	Thr	His	Arg	Tyr	Pro	Asp	Arg	Val	Leu	Phe
			115				120					125			

Leu Val Thr Asn Gln Cys Ser Val Tyr Cys Arg Tyr Cys Thr Arg Arg
 130 135 140

Arg Phe Ser Gly Gln Ile Gly Met Gly Val Pro Lys Lys Gln Leu Asp
 145 150 155 160

Ala Ala Ile Ala Tyr Ile Arg Glu Thr Pro Glu Ile Arg Asp Cys Leu
 165 170 175

Ile Ser Gly Gly Asp Gly Leu Leu Ile Asn Asp Gln Ile Leu Glu Tyr
 180 185 190

Ile Leu Lys Glu Leu Arg Ser Ile Pro His Leu Glu Val Ile Arg Ile
 195 200 205

Gly Thr Arg Ala Pro Val Val Phe Pro Gln Arg Ile Thr Asp His Leu
 210 215 220

Cys Glu Ile Leu Lys Lys Tyr His Pro Val Trp Leu Asn Thr His Phe
 225 230 235 240

Asn Thr Ser Ile Glu Met Thr Glu Glu Ser Val Glu Ala Cys Glu Lys
 245 250 255

Leu Val Asn Ala Gly Val Pro Val Gly Asn Gln Ala Val Val Leu Ala
 260 265 270

Gly Ile Asn Asp Ser Val Pro Ile Met Lys Lys Leu Met His Asp Leu
 275 280 285

Val Lys Ile Arg Val Arg Pro Tyr Tyr Ile Tyr Gln Cys Asp Leu Ser
 290 295 300

Glu Gly Ile Gly His Phe Arg Ala Pro Val Ser Lys Gly Leu Glu Ile
 305 310 315 320

Ile Glu Gly Leu Arg Gly His Thr Ser Gly Tyr Ala Val Pro Thr Phe
 325 330 335

Val Val His Ala Pro Gly Gly Gly Gly Lys Ile Ala Leu Gln Pro Asn
 340 345 350

Tyr Val Leu Ser Gln Ser Pro Asp Lys Val Ile Leu Arg Asn Phe Glu
 355 360 365

Gly Val Ile Thr Ser Tyr Pro Glu Pro Glu Asn Tyr Ile Pro Asn Gln
 370 375 380

Ala Asp Ala Tyr Phe Glu Ser Val Phe Pro Glu Thr Ala Asp Lys Lys
 385 390 395 400

Glu Pro Ile Gly Leu Ser Ala Ile Phe Ala Asp Lys Glu Val Ser Phe
 405 410 415

Thr Pro Glu Asn Val Asp Arg Ile Lys Arg Arg Glu Ala Tyr Ile Ala
 420 425 430

Asn Pro Glu His Glu Thr Leu Lys Asp Arg Arg Glu Lys Arg Asp Gln
 435 440 445

Leu Lys Glu Lys Lys Phe Leu Ala Gln Gln Lys Lys Gln Lys Glu Thr
 450 455 460

Glu Cys Gly Gly Asp Ser Ser
 465 470

<210> 25
 <211> 1251
 <212> DNA
 <213> Porphyromonas gingivalis

<220>
 <221> CDS
 <222> (1) .. (1248)

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Met Ala Glu Ser Arg Arg Lys Tyr Tyr Phe Pro Asp Val Thr Asp Glu	
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caa tgg tac gac tgg cat tgg cag gtc ctc aat cga att gag acg ctc	96
Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu	
20 25 30	
gac cag ctg aaa aag tac gtt aca ctc acc gct gaa gaa gaa gag gga	144
Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Glu Gly	
35 40 45	
gta aaa gaa tcg ccc aaa gta ctc cga atg gct atc aca cct tat tat	192
Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr	

50	55	60	
ttg agt ttg ata gac ccc gag aat cct aat tgt ccg att cgt aaa caa			240
Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln			
65	70	75	80
gcc att cct act caa cag gaa ctg gta cgt gct cct gaa gat cag gta			288
Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val			
	85	90	95
gac cca ctt agt gaa gat gaa gat tcg ccc gta ccc gga ctg act cat			336
Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His			
	100	105	110
cgt tat ccg gat cgt gta ttg ttc ctt atc acg gac aaa tgt tcg atg			384
Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met			
	115	120	125
tac tgt cgt cat tgt act cgc cgt cgc ttc gca gga cag aaa gat gct			432
Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala			
	130	135	140
tct tct cct tct gag cgc atc gat cga tgc att gac tat ata gcc aat			480
Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn			
	145	150	155
aca ccg aca gtc cgc gat gtt ttg cta tcg gga ggc gat gcc ctc ctt			528
Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu			
	165	170	175
gtc agc gac gaa cgc ttg gaa tac ata ttg aag cgt ctg cgc gaa ata			576
Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile			
	180	185	190
cct cat gtg gag att gtt cgt ata gga agc cgt acg ccg gta gtc ctc			624
Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu			
	195	200	205
cct cag cgt ata acg cct caa ttg gtg gat atg ctc aaa aaa tat cat			672
Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His			
	210	215	220
ccg gtg tgg ctg aac act cac ttc aac cac ccg aat gaa gtt acc gaa			720
Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu			
	225	230	240
gaa gca gta gag gct tgt gaa aga atg gcc aat gcc ggt att ccg ttg			768
Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu			
	245	250	255
ggt aac caa acg gtt tta ttg cgt gga atc aat gat tgt aca cat gtg			816
Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val			
	260	265	270
atg aag aga ttg gta cat ttg ctg gta aag atg cgt gtg cgt cct tac			864
Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr			
	275	280	285

tat ata tat gta tgc gat ctt tcg ctt gga ata ggt cat ttc cgc acg	912
Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr	
290 295 300	
ccg gta tct aaa gga atc gaa att atc gaa aat ttg cgc gga cac acc	960
Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr	
305 310 315 320	
tcg ggc tat gca gtt cct acc ttt gtg gta ggt gct ccg ggg ggt ggt	1008
Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly Gly	
325 330 335	
ggt aag ata cct gta acg ccg aac tat gtt gta tct cag tcc cca cga	1056
Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg	
340 345 350	
cat gtg gtt ctt cgc aat tat gaa ggt gtt atc aca acc tat acg gag	1104
His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu	
355 360 365	
ccg gag aat tat cat gag gag tgc gat tgt gag gac tgt cga gcc ggt	1152
Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly	
370 375 380	
aag cat aaa gag ggt gta gct gca ctt tcc gga ggt cag cag ttg gct	1200
Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala	
385 390 395 400	
atc gag cct tcc gac tta gct cgc aaa aaa cgc aag ttt gat aag aac	1248
Ile Glu Pro Ser Asp Leu Ala Arg Lys Lys Arg Lys Phe Asp Lys Asn	
405 410 415	
tga	1251

<210> 26
 <211> 416
 <212> PRT
 <213> Porphyromonas gingivalis

<400> 26

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Gln Trp Tyr Asp Trp His Trp Gln Val Leu Asn Arg Ile Glu Thr Leu
20 25 30

Asp Gln Leu Lys Lys Tyr Val Thr Leu Thr Ala Glu Glu Glu Glu Gly
35 40 45

Val Lys Glu Ser Pro Lys Val Leu Arg Met Ala Ile Thr Pro Tyr Tyr
50 55 60

Leu Ser Leu Ile Asp Pro Glu Asn Pro Asn Cys Pro Ile Arg Lys Gln
 65 70 75 80

Ala Ile Pro Thr Gln Gln Glu Leu Val Arg Ala Pro Glu Asp Gln Val
 85 90 95

Asp Pro Leu Ser Glu Asp Glu Asp Ser Pro Val Pro Gly Leu Thr His
 100 105 110

Arg Tyr Pro Asp Arg Val Leu Phe Leu Ile Thr Asp Lys Cys Ser Met
 115 120 125

Tyr Cys Arg His Cys Thr Arg Arg Arg Phe Ala Gly Gln Lys Asp Ala
 130 135 140

Ser Ser Pro Ser Glu Arg Ile Asp Arg Cys Ile Asp Tyr Ile Ala Asn
 145 150 155 160

Thr Pro Thr Val Arg Asp Val Leu Leu Ser Gly Gly Asp Ala Leu Leu
 165 170 175

Val Ser Asp Glu Arg Leu Glu Tyr Ile Leu Lys Arg Leu Arg Glu Ile
 180 185 190

Pro His Val Glu Ile Val Arg Ile Gly Ser Arg Thr Pro Val Val Leu
 195 200 205

Pro Gln Arg Ile Thr Pro Gln Leu Val Asp Met Leu Lys Lys Tyr His
 210 215 220

Pro Val Trp Leu Asn Thr His Phe Asn His Pro Asn Glu Val Thr Glu
 225 230 235 240

Glu Ala Val Glu Ala Cys Glu Arg Met Ala Asn Ala Gly Ile Pro Leu
 245 250 255

Gly Asn Gln Thr Val Leu Leu Arg Gly Ile Asn Asp Cys Thr His Val
 260 265 270

Met Lys Arg Leu Val His Leu Leu Val Lys Met Arg Val Arg Pro Tyr
 275 280 285

Tyr Ile Tyr Val Cys Asp Leu Ser Leu Gly Ile Gly His Phe Arg Thr
 290 295 300

Pro Val Ser Lys Gly Ile Glu Ile Ile Glu Asn Leu Arg Gly His Thr
 305 310 315 320

Ser Gly Tyr Ala Val Pro Thr Phe Val Val Gly Ala Pro Gly Gly Gly
 325 330 335

Gly Lys Ile Pro Val Thr Pro Asn Tyr Val Val Ser Gln Ser Pro Arg
 340 345 350

His Val Val Leu Arg Asn Tyr Glu Gly Val Ile Thr Thr Tyr Thr Glu
 355 360 365

Pro Glu Asn Tyr His Glu Glu Cys Asp Cys Glu Asp Cys Arg Ala Gly
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Lys His Lys Glu Gly Val Ala Ala Leu Ser Gly Gly Gln Gln Leu Ala
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 Ala Ala Asn Leu Leu Lys Ala Gly His Arg Val Asn Val Phe Asp Leu
 20 25 30
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 Gln Pro Lys Ala Val Leu Gly Leu Val Glu Gln Gly Ala Gln Gly Ala
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 gat agc gcc ttg cag tgc tgc gaa ggc gcc gaa gtg gtg atc agc atg 192

Asp	Ser	Ala	Leu	Gln	Cys	Cys	Glu	Gly	Ala	Glu	Val	Val	Ile	Ser	Met	
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ctg	ccg	gcc	ggg	cag	cac	gtg	gaa	agc	ctg	tat	ctc	ggc	gac	gac	ggc	240
Leu	Pro	Ala	Gly	Gln	His	Val	Glu	Ser	Leu	Tyr	Leu	Gly	Asp	Asp	Gly	
65					70					75					80	
ctg	ctc	gcg	cgg	gtc	gcc	ggc	aag	ccc	ctg	ctg	atc	gac	tgc	tcg	acc	288
Leu	Leu	Ala	Arg	Val	Ala	Gly	Lys	Pro	Leu	Leu	Ile	Asp	Cys	Ser	Thr	
				85					90					95		
atc	gcc	ccg	gag	acc	gcg	cgc	aag	gtc	gcc	gag	gcc	gcc	gcg	gcg	aag	336
Ile	Ala	Pro	Glu	Thr	Ala	Arg	Lys	Val	Ala	Glu	Ala	Ala	Ala	Ala	Lys	
			100					105					110			
ggc	ctg	acc	ctg	ctc	gac	gcg	ccg	gtt	tcc	ggc	ggc	gtc	ggc	ggc	gcc	384
Gly	Leu	Thr	Leu	Leu	Asp	Ala	Pro	Val	Ser	Gly	Gly	Val	Gly	Gly	Ala	
		115						120				125				
cgc	gcc	ggc	acc	ctg	agc	ttc	atc	gtc	ggc	ggc	ccc	gcc	gaa	ggc	ttc	432
Arg	Ala	Gly	Thr	Leu	Ser	Phe	Ile	Val	Gly	Gly	Pro	Ala	Glu	Gly	Phe	
		130				135					140					
gcg	cgg	gcc	cgg	ccg	gtc	ctc	gag	aac	atg	ggc	cgg	aac	atc	ttc	cac	480
Ala	Arg	Ala	Arg	Pro	Val	Leu	Glu	Asn	Met	Gly	Arg	Asn	Ile	Phe	His	
145					150				155						160	
gcc	ggc	gat	cac	ggc	gcc	ggc	cag	gtg	gcg	aag	atc	tgc	aac	aac	atg	528
Ala	Gly	Asp	His	Gly	Ala	Gly	Gln	Val	Ala	Lys	Ile	Cys	Asn	Asn	Met	
				165				170						175		
ctc	ctc	ggc	atc	ctc	atg	gcc	ggc	acc	gcc	gag	gcc	ctg	gcg	ctg	ggg	576
Leu	Leu	Gly	Ile	Leu	Met	Ala	Gly	Thr	Ala	Glu	Ala	Leu	Ala	Leu	Gly	
			180					185					190			
gtg	aag	aac	ggc	ctc	gac	ccg	gcg	gtg	ctg	tcc	gag	gtg	atg	aag	cag	624
Val	Lys	Asn	Gly	Leu	Asp	Pro	Ala	Val	Leu	Ser	Glu	Val	Met	Lys	Gln	
		195					200					205				
agt	tcc	ggc	ggc	aac	tgg	gcg	ctg	aac	ctc	tac	aac	ccc	tgg	ccc	ggg	672
Ser	Ser	Gly	Gly	Asn	Trp	Ala	Leu	Asn	Leu	Tyr	Asn	Pro	Trp	Pro	Gly	
		210				215					220					
gtg	atg	ccg	cag	gcg	ccg	gcg	agc	aac	ggc	tat	gcc	ggc	ggc	ttc	cag	720
Val	Met	Pro	Gln	Ala	Pro	Ala	Ser	Asn	Gly	Tyr	Ala	Gly	Gly	Phe	Gln	
225					230					235					240	
gtg	cgc	ctg	atg	aac	aag	gac	ctc	ggc	ctg	gcg	ctg	gcc	aac	gcc	cag	768
Val	Arg	Leu	Met	Asn	Lys	Asp	Leu	Gly	Leu	Ala	Leu	Ala	Asn	Ala	Gln	
				245				250						255		
gcg	gtg	cag	gcc	tcg	acg	ccg	ctc	ggc	gcg	ctg	gcg	cgc	aac	ctg	ttc	816
Ala	Val	Gln	Ala	Ser	Thr	Pro	Leu	Gly	Ala	Leu	Ala	Arg	Asn	Leu	Phe	
			260					265					270			
agc	ctg	cac	gcc	cag	gcc	gat	gcc	gag	cac	gag	ggg	ctg	gac	ttc	tcc	864
Ser	Leu	His	Ala	Gln	Ala	Asp	Ala	Glu	His	Glu	Gly	Leu	Asp	Phe	Ser	

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897

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Gln Pro Lys Ala Val Leu Gly Leu Val Glu Gln Gly Ala Gln Gly Ala
35 40 45

Asp Ser Ala Leu Gln Cys Cys Glu Gly Ala Glu Val Val Ile Ser Met
50 55 60

Leu Pro Ala Gly Gln His Val Glu Ser Leu Tyr Leu Gly Asp Asp Gly
65 70 75 80

Leu Leu Ala Arg Val Ala Gly Lys Pro Leu Leu Ile Asp Cys Ser Thr
85 90 95

Ile Ala Pro Glu Thr Ala Arg Lys Val Ala Glu Ala Ala Ala Lys
100 105 110

Gly Leu Thr Leu Leu Asp Ala Pro Val Ser Gly Gly Val Gly Gly Ala
115 120 125

Arg Ala Gly Thr Leu Ser Phe Ile Val Gly Gly Pro Ala Glu Gly Phe
130 135 140

Ala Arg Ala Arg Pro Val Leu Glu Asn Met Gly Arg Asn Ile Phe His
145 150 155 160

Ala Gly Asp His Gly Ala Gly Gln Val Ala Lys Ile Cys Asn Asn Met
165 170 175

Leu Leu Gly Ile Leu Met Ala Gly Thr Ala Glu Ala Leu Ala Leu Gly
180 185 190

Val Lys Asn Gly Leu Asp Pro Ala Val Leu Ser Glu Val Met Lys Gln
195 200 205

Ser Ser Gly Gly Asn Trp Ala Leu Asn Leu Tyr Asn Pro Trp Pro Gly
210 215 220

Val Met Pro Gln Ala Pro Ala Ser Asn Gly Tyr Ala Gly Gly Phe Gln
225 230 235 240

Val Arg Leu Met Asn Lys Asp Leu Gly Leu Ala Leu Ala Asn Ala Gln
245 250 255

Ala Val Gln Ala Ser Thr Pro Leu Gly Ala Leu Ala Arg Asn Leu Phe
260 265 270

Ser Leu His Ala Gln Ala Asp Ala Glu His Glu Gly Leu Asp Phe Ser
275 280 285

Ser Ile Gln Lys Leu Tyr Arg Gly Lys Asp
290 295